One of the earliest studies publishing sequencing data (Illumina) from two SARS-Cov2 patients in Wuhan failed to identify potentially pathogenic bacteria using the program Metaphlan2, when they clearly exist

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Letter

It is increasingly being evident that bacterial coinfection is playing an important role in SARS-Cov2 [1–4], explaining hydroxychloroquine and azithromycin working in clinical trials [5]. Previously, I have analyzed the metagenomes in patients from China [6,7], San Diego [8] and Brazil [9] - showing many bacterial species (sometimes many unknowns), and Prevotella immune-suppression genes taking over [6].

Failure to identify pathogenic bacteria using Metaphlan2

One of the earliest studies publishing sequencing data (Illumina) from two SARS-Cov patients in Wuhan [10] wrote ‘*bacterial pathogen identification was carried out by using the Metaphlan2 program, which revealed Capnocytophaga sp and Veillonella sp in sample 2 and none in sample 1, and both bacteria identified were not known for their pathogenicity. Collectively, coronavirus is likely to be the main microbial pathogen*’ [10]. This is clearly wrong - Capnocytophaga and Lautropia are there, and also so many other pathogenic species (Table 1). Sequences and full list of bacterial species are in SIstudy3MNGS. And Capnocytophaga, found in the saliva of humans, dogs and cats can be pathogenic [11]. Another observation is that bacteria will high counts are mostly anaerobic.

Table 1: **Bacterial species identified in two patients from Wuhan:** The original paper stated that ‘bacterial pathogen identification was carried out by using the Metaphlan2 program, which revealed Capnocytophaga sp and Veillonella sp in sample 2 and none in sample 1, and both bacteria identified were not known for their pathogenicity’ This is clearly wrong - Capnocytophaga and Lautropia are there, but there are so many other pathogenic species. Also Capnocytophaga, found in the saliva of humans, dogs and cats can be pathogenic [11]. There are many more species, just listed top 10 here.

	Patient1	Patient2
Accid: Total	SRR10903402 676694	SRR10903401 476632
	Bacteria/ Reads per million	Bacteria/ Reads per million
1	Capnocytophaga 1195.6	Prevotella 247
2	Streptococcus 694.4	Lautropia 236
3	Prevotella 578.9	Veillonella 132
4	Lautropia 512.4	Schaalia 20.5
5	Lactobacillus 161.7	Escherichia 17.5
6	Veillonella 157.5	Streptococcus 16.5
7	Mycoplasma 107.1	Campylobacter 14
8	Schaalia 81.9	Megasphaera 4.5
9	Escherichia 49	Acinetobacter 3.5
10	Rothia 37.8	Actinomyces 3.5

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